APPROVED O.G. FIG.
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	-				
				CCGCCTAGCA	
				TTCCCGGCGT	
101				CCGCGGCCGT	
151				GCCCGGGCCG	
201	GCGGGCGCCG	CGGGAAGACC	TTGGCGCGGG	GCGGCGGGCC	GGGCCAGGCC
251	ATGCGGGCCG	AGTGAGCCGG	CGCCCGCAGC	CCGCGGCGCG	GCATGGCTTC
301				GCCGCCGCCG	
351	CCGCGCGCCT	GCTACTGCTA	CTGCTGCTGC	CGCTGCTGCT	GCCTCTGGCG
				CCCCGGCCGC	
451	CCCGCCGCTC	TCCATCATGG	GCCTCATGCC	GCTCACCAAG	GAGGTGGCCA
				CCGTGGAACT	
551	CAGATCCGCA	ACGAGTCACT	CCTGCGCCCC	TACTTCCTCG	ACCTGCGGCT
601	CTATGACACG	GAGTGCGACA	ACGCAAAAGG	GTTGAAAGCC	TTCTACGATG
				TGTTTGGAGG	
701	TCCGTCACAT	CCATCATTGC	AGAGTCCCTC	CAAGGCTGGA	ATCTGGTGCA
751	GCTTTCTTTT	GCTGCAACCA	CGCCTGTTCT	AGCCGATAAG	AAAAAATACC
801	CTTATTTCTT	TCGGACCGTC	CCATCAGACA	ATGCGGTGAA	TCCAGCCATT
851	CTGAAGTTGC	TCAAGCACTA	CCAGTGGAAG	CGCGTGGGCA	CGCTGACGCA
901	AGACGTTCAG	AGGTTCTCTG	AGGTGCGGAA	TGACCTGACT	GGAGTTCTGT
951	ATGGCGAGGA	CATTGAGATT	TCAGACACCG	AGAGCTTCTC	CAACGATCCC
1001	TGTACCAGTG	TCAAAAAGCT	GAAGGGGAAT	GATGTGCGGA	TCATCCTTGG
1051	CCAGTTTGAC	CAGAATATGG	CAGCAAAAGT	GTTCTGTTGT	GCATACGAGG
				TCATTCCGGG	
				GCCAACTCAT	
1201				CTACATTGGC	
1251				TCTCAGGAAA	
				TCAGGCGTGG	
				GGTCATCGCC	
				GCCGGCACCA	
				AGGATCATCC	
1501				TCAAGTTGTA	
1551				AATTTCAAGA	
					AGATCATCAA
					AAGACCATCA
					CATCCTCTCT
					TCTTCTTCAA
					CCATACATGA
					CATATTTCTC
					AAACACTTTG
					GCTTTTGGGG
					AAATGTGAAA
					TCGTGGGGGG
					GCTGTGGACC
2151	CCCTGCGAAG	GACAGTGGAG	AAGTACAGCA	A TGGAGCCGGA	CCCAGCAGGA

FIG.1A

J.G. FIG.	CLASS SUBCLASS	
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2201	CGGGATATCT	CCATCCGCCC	TCTCCTGGAG	CACTGTGAGA	ACACCCATAT
2251	GACCATCTGG	CTTGGCATCG	TCTATGCCTA	CAAGGGACTT	CTCATGTTGT
2301	TCGGTTGTTT	CTTAGCTTGG	GAGACCCGCA	ACGTCAGCAT	CCCCGCACTC
2351	AACGACAGCA	AGTACATCGG	GATGAGTGTC	TACAACGTGG	GGATCATGTG
2401	CATCATCGGG	GCCGCTGTCT	CCTTCCTGAC	CCGGGACCAG	CCCAATGTGC
2451	AGTTCTGCAT	CGTGGCTCTG	GTCATCATCT	TCTGCAGCAC	CATCACCCTC
2501	TGCCTGGTAT	TCGTGCCGAA	GCTCATCACC	CTGAGAACAA.	ACCCAGATGC
2551		AACAGGCGAT			
2601		GTCCACCTCG			
2651		GCCTACAGTC			
2701		AAAGACTTGG			
2751		CACCTACATT			
2801		TGGGAAACTT			
2851		CACCTCGATC			
2901		AACATGCAAA			
2951		GTCGGCTGTC			
3001		ATCGGAGGCG			
3051		CAGCCCCCGC			
3101		GCCTGTAAGG			
3151	TGACAGAACC	ACACTGGGCA	GAGGGGTCTG		
3201	CTGGCTGCGG	AGAAGCTGGG	CACCATGGCT		GACCACTCGG
3251	ATGGCACTCA	GGTGGACAGG	ACGGGGCAGG		GCACCTGACC
3301		TTTGTGAAGT			GAGGAACGGA
3351		CTTCCTTAAC			
3401	AATTCCACCA	CACTGGCGGC	CCGCGCTTGS	TCSTAATCAT	GGTCATAACT
3451	GTTTCCTGTG	TTGAAATTGT	TATCCGCTCC		

FIG.1B

APPROVED O.G. FIG.

BY CLASS SUBCLASS

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1 MASPRSSGQP GPPPPPPPPP ARLLLLLLP LLLPLAPGAW GWARGAPRPP 51 PSSPPLSIMG LMPLTKEVAK GSIGRGVLPA VELAIEQIRN ESLLRPYFLD 101 LRLYDTECDN AKGLKAFYDA IKYGPNHLMV FGGVCPSVTS IIAESLQGWN 151 LVQLSFAATT PVLADKKKYP YFFRTVPSDN AVNPAILKLL KHYQWKRVGT 201 LTQDVQRFSE VRNDLTGVLY GEDIEISDTE SFSNDPCTSV KKLKGNDVRI 251 ILGQFDQNMA AKVFCCAYEE NMYGSKYQWI IPGWYEPSWW EQVHTEANSS 301 RCLRKNLLAA MEGYIGVDFE PLSSKQIKTI SGKTPQQYER EYNNKRSGVG 351 PSKFHGYAYD GIWVIAKTLQ RAMETLHASS RHQRIQDFNY TDHTLGRIIL 401 NAMNETNFFG VTGQVVFRNG ERMGTIKFTQ FQDSREVKVG EYNAVADTLE 451 IINDTIRFQG SEPPKDKTII LEQLRKISLP LYSILSALTI LGMIMASAFL 501 FENIKNRNOK LIKMSSPYMN NLIILGGMLS YASIFLEGLD GSFVSEKTFE 551 TLCTVRTWIL TVGYTTAFGA MFAKTWRVHA IFKNVKMKKK IIKDOKLLVI 601 VGGMLLIDLC ILICWQAVDP LRRTVEKYSM EPDPAGRDIS IRPLLEHCEN 651 THMTIWLGIV YAYKGLLMLF GCFLAWETRN VSIPALNDSK YIGMSVYNVG 701 IMCIIGAAVS FLTRDQPNVQ FCIVALVIIF CSTITLCLVF VPKLITLRTN 751 PDAATQNRRF QFTQNQKKED SKTSTSVTSV NQASTSRLEG LQSENHRLRM 801 KITELDKOLE EVTMQLQDTP EKTTYIKQNH YQELNDILNL GNFTESTDGG 851 KAILKNHLDQ NPQLQWNTTE PSRTCKDPIE DINSPEHIQR RLSLQLPILH 901 HAYLPSIGGV DASCVSPCVS PTASPRHRHV PPSFRVMVSG L

FIG.2

APPROVED O.G. FIG.

BY CLASS SUBCLASS
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Sequence: LPLLLPLAPGAWG-WARGAPRPPPSSPPLSIMGLMPLTKEVAKGSIGRGVLPAVELAIEQIRNE |(signal) |(mature peptide) | 42

Other entries above 3.50

Score 11.1 at residue 39

Sequence: LLLLPLLLPLAPG-AWGWARGAPRPPPSSPPLSIMGLMPLTKEVAKGSIGRGVLPAVELAIEQI |(signal) |(mature peptide) 26 39

Score 8.6 at residue 38

Sequence: LLLLLPLLLPLAP-GAWGWARGAPRPPPSSPPLSIMGLMPLTKEVAKGSIGRGVLPAVELAIEQ |(signal) | (mature peptide) 25 38

Score 8.1 at residue 35

Sequence: RLILLLLPLLLP-LAPGAWGWARGAPRPPPSSPPLSIMGLMPLTKEVAKGSIGRGVLPAVELA |(signal) |(mature peptide) 22 35

Score 7.9 at residue 36

Sequence: LILLLLPLLLPL-APGAWGWARGAPRPPPSSPPLSIMGLMPLTKEVAKGSIGRGVLPAVELAI |(signal) |(mature peptide) 23 36

Score 6.2 at residue 9

Score 5.7 at residue 46

Sequence: LPLAPGAWGWARG-APRPPPSSPPLSIMGLMPLTKEVAKGSIGRGVLPAVELAIEQIRNESLLR |(signal) |(mature peptide) 33 46

Score 5.6 at residue 747

Sequence: ITLCLVFVPKLIT-LRTNPDAATQNRRFQFTQNQKKEDSKTSTSVTSVNQASTSRLEGLQSENH |(signal) |(mature peptide) 734 747

Score 5.0 at residue 44

Sequence LLLPLAPGAWGWA-RGAPRPPPSSPPLSIMGLMPLTKEVAKGSIGRGVLPAVELAIEQIRNESL |(signal) |(mature peptide) 31 44

Score 4.9 at residue 497

FIG.3A



Sequence: ILSALTILGMIMA-SAFLFFNIKNRNQKLIKMSSPMNNLIILGGMLSYASIFLFGLDGSFVSE [(signal) | (mature peptide)

484 497

Score 4.5 at residue 141

Sequence: LMVFGGVCPSVTS-IIAESLQGWNLVQLSFAATTPVLADKKKYPYFFRTVPSDNAVNPAILKLL |(signal) |(mature peptide)

128 141

Score 4.4 at residue 734

Sequence: FCIVALVIIFCST-ITLCLVFVPKLITLRTNPDAATQNRRFQFTQNQKKEDSKTSTSVTSVNQA |(signal) |(mature peptide)

721 734

Score 4.1 at residue 165

Sequence: VQLSFAATTPVLA-DKKKYPYFFRTVPSDNAVNPAILKLLKHYQWKRVGTLTQDVQRFSEVRND

|(signal) |(mature peptide)

152 165

Score 3.6 at residue 158

Sequence: SLQGWNLVQLSFA-ATTPVLADKKKYPYFFRTVPSDNAVNPAILKLLKHYQWKRVGTLTQDVQR

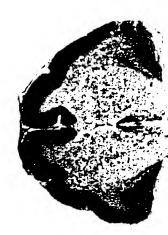
|(signal) |(mature peptide)

145 158

FIG.3B

CLASS SUBCLASS APPROVED O.G. FIG. DRAFTSMAN ¥

Distribution of mRNA for EST z43654 in squirrel monkey brain.

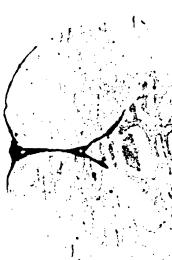




at level of caudate and putamen

FIG.4

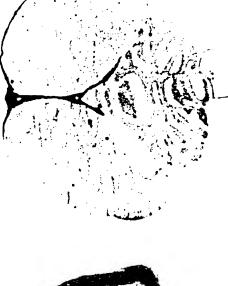
at level of thalamus and hippocampus



example of cold displayed



at level of cerebellum and occipital cortex



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Melanophores 1- FLAG-HG20/pcDNA 3.1 2- pcDNA 3.1 COS-7

4- pcDNA 3.1

3- FLAG-HG20/pcDNA 3.1

3- Mouse GABA<sub>B</sub>/ pcDNA 3:1

4- pcDNA 3:1

FIG.5A

2- FLAG-HG20/pcDNA 3:1

1- HG20/PCR 3.1

30 —

FIG.5B

0.G. FIG.	CLASS SUBCLASS	
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PLTKEVAK-GSIGR-GVLPAVELAIEQIRNESLLRPYFLDLRLYDTECDNAKGLKAFYDA :.: ::: :: :X : PVTGPVAQYGDMQRAGALMAIEQINKAGGVNGAQLEGVIYDDACDPKQAVAVANKV
IKYGPNHLMVFGGVCPSVTSIIAESLQGWNLVQLSFAATTPVLADKKKYPYFFRTVPSDN
AVNPAILKLL-KHYQWKRVGTLTQDVQRFSE-VRNDLTGVLYGEDIEISDTESFSND .:. : :: :: :: :: :: :: :: :: :: :: ::
PCTSVKKLKGNDVRII-LGQFDQNM : : : : FNALISKLKKAGVQFVYFGGYHPEM

FIG.6

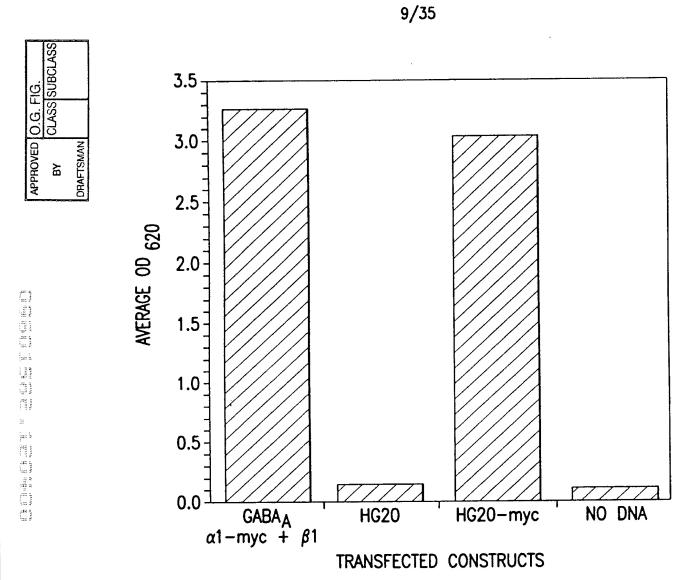


FIG.7

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APPROVED O.G. FIG.	BY CLASS SUBCLASS	DRAFTSMAN
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			•			
69	143	218	290	365	440	512
75	149	224	299	372	446	519
75	150	225	300	375	450	525
MGPGGPCTPVGWPLPLLLVMAAGVAPVWASHSPHLPRPHPRVPPHPSSERRAVYIGALFPMSGGWP-GGQ MASPRSSGQPGRPPPPPPPARLILLLLLLLLPLLPGAWGWARGAPRPPSSPPLSIMGLMPLTKEVAKGSIGR MG.P.PA	ACQPAVEMALEDVNSRRDILPDYELKLIHHDSKCDPGQATKYLYELLYNDPIKIILMPG-CSSVSTLVAEAARMW GVLPAVELAIEQIRN-ESLLRPYFLDLRLYDTECDNAKGLKAFYDAIKYGPNHLMVFGGVCPSVTSIIAESLQGW SPAVE.A.EL.Y.L.LDCDKYBG.C.SVAEW	NLIVLSYGSSSPALSNRQRFPTFFRTHPSATLHNPTRVKLFEKWGWKKIATIQQTTEVFTSTLDDLEERVKEAGI NLVQLSFAATTPVLADKKKYPYFFRTVPSDNAVNPAILKLLKHYQWKRVGTLTQDVQRFSEVRNDLTGVLYGEDI S NLLSP.FFRT.PSNPKLWKTQFDLI	b EITFRQSFFSDPAVPVKNLKRQDARIIVGLFYETEARKVFCEVYKERLFGKKYVWFLIGWYADNWFKTYDPS EISDTESFSNDPCTSVKKLKGNDVRIILGQFDQNMAAKVFCCAYEENMYGSKYQWIIPGWYEPSWWEQVHTEANS s EISFDPVK.LKD.RII.G.FA.KVFCY.EG.KY.WGWYWTS	b INCTVEEMTEAVEGHITTEIVMLNPANTRSISNMTSQEFVEKLTKRLKRHPEETGGFQEAPLAYDAIWALALALN SRCLRKNLLAAMEGYIGVDFEPLSSKQIKTISGKTPQQY-EREYNN-KRSGVGPSKFHGYAYDGIWVIAKTLQRA sCA.EG.ILIST.QEKRFA.EG.IAL	<pre>b KTSGGGGRSGVRLEDFNYNNQTITDQIYRAMNSSSFEGVSGHVVFDASGSRMAWTLIEQLQGGSYKKIGYYDSTK     METLHASSRHQRIQDFNYTDHTLGRIILNAMNETNFFGVTGQVVFR-NGERMGTIKFTQFQDSREVKVGEYNAVA s</pre>	b DDLSWSKTDKWIGGSPPADQTLVIKTFRFLSQKLFISVSVLSSLGIVLAVVCLSFNIYNSHVRYIQNSQPNL DTLEIINDTIRFQGSEPPKDKTIILEQLRKISLPLYSILSALTILGMIMASAFLFFNIKNRNQKLIKMSSPYM IS D.L
GABA-BR1b	GABA-BR1b	GABA-BR1b	GABA-BR1b	GABA-BR1b	GABA-3R1b	GABA-BR1b
HG20	HG20	HG20	HG20	HG20	HG20	HG20
Consensus	Consensus	Consensus	Consensus	Consensus	Consensus	Consensus

FIG.8A

APPROVED O.G. FIG.

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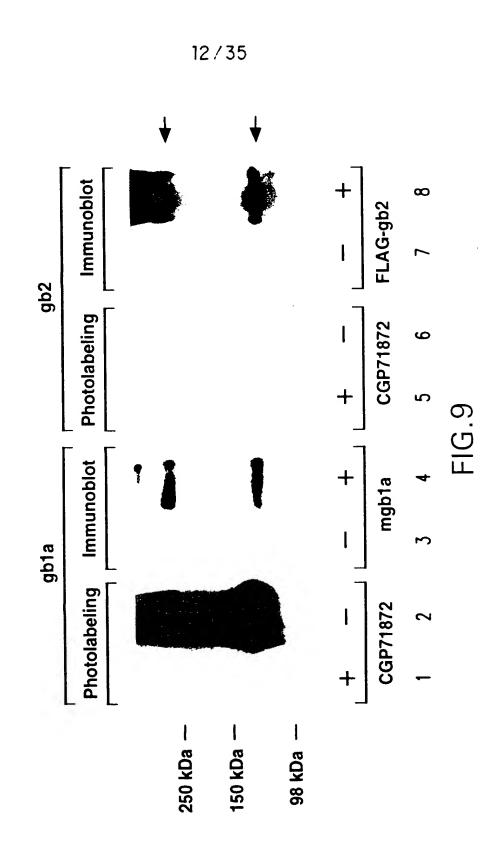
(KI 591 .K. 600	KGL 662 KGL 666 KGL 675	LFV 737 VFV 741 .FV 750	784 MQL 816 825	QRR 891	844 941 950
HG20 NNLIILGGMLSYASIFLFGLDGSFVSEKTFETLCTVRTWILTVGYTTAFGAMFAKTWRVHAIFKNVKMK-KKI Consensus NNLGLAFGLDGFCR.W.LGG.MF.K.W.VHFKKK.	GABA-BRID LEPWKLYATVGLLVGMDVLTLAIWQIVDPLHRTIETFAKEEPKEDIDVSILPQLEHCSSKKMNTWLGIFYGYKGL HG20 IKDQKLLVIVGGMLLIDLCILICWQAVDPLRRTVEKYSMEPDPAGRDISIRPLLEHCENTHMTIWLGIVYAYKGL ConsensusKLVGDLWQ.VDPL.RT.EED.SI.P.LEHCMWLGI.Y.YKGL	GABA-BRID LLLLGIFLAYETKSVSTEKINDHRAVGMAIYNVAVLCLITAPVTMILSSQQDAAFAFASLAIVFSSYITLVVLFV HG20 LMLFGCFLAWETRNVSIPALNDSKYIGMSVYNVGIMCIIGAAVSFLTRDQPNVQFCIVALVIIFCSTITLCLVFV Consensus L.L.G.FLA.ETVSNDGMYNVC.I.A.VQFL.I.F.S.ITLFV	GABA-BRIb PKMRRLITRGEWQSETQDTMKTGSS-TNNNEEEKSRLLEKENRELEKI HG20 PKLITLRTNPDAATQNRRFQFTQNQKKEDSKTSTSVTSVNQASTSRLEGLQSENHRLRMKITELDKDLEEVTMQL Consensus PKL.TQKTS.TNSRLL.E	GABA-BRIDIAEKEERVSELONGURGRQQLRSRRHPPTPPDPSGG	JLPR-GPSEPPORLSCDGSRVHLLYK LSLQLPILHHAYLPSIGGVDASCVSPCVSPTASPRHRHVPPSFRVMVSGL SLPGCRR
HG20 Consensus	GABA-BR1t HG20 Consensus	GABA-BR11 HG20 Consensu	GABA-BRI HG20 Consensu	GABA-BR1 HG20 Consensu	GABA-BR1b HG20 LSLQLP Consensus

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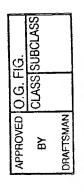
## FIG.8B

APPROVED O.G. FIG.
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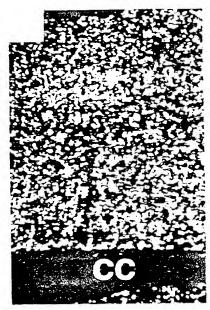


FIG.10A

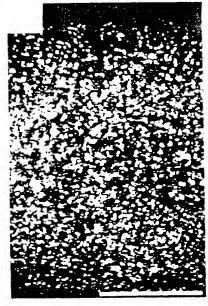


FIG.10B



FIG.10C

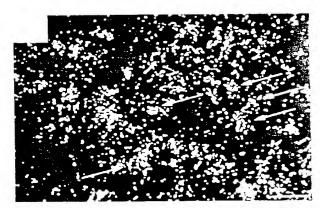


FIG.10D

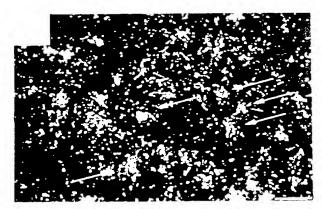
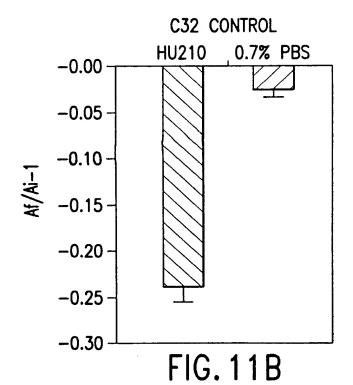


FIG.10E

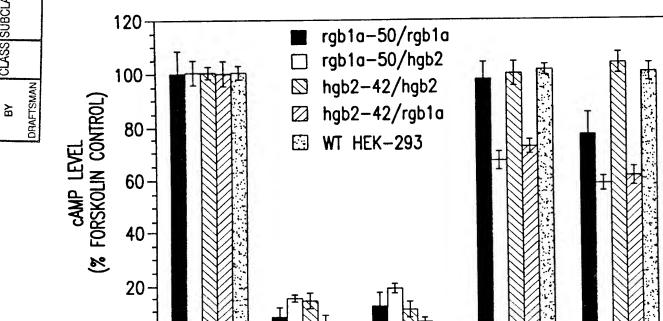
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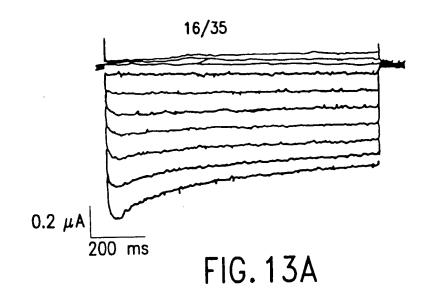
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FIG. 12

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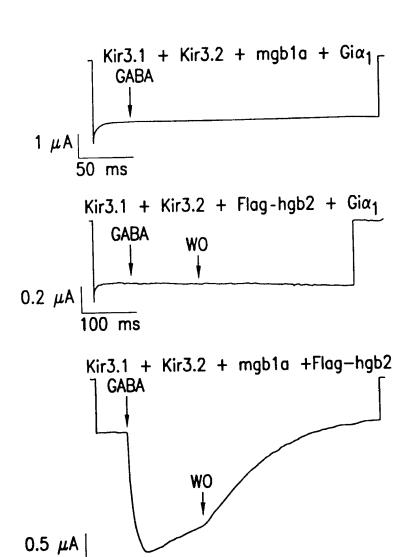


FIG. 13B

50 ms



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pcDNA3.1 FLAG-gb2

mgb1a

mgb1a + FLAG-gb2

4

250 kDa —

150 kDa —

→ gb1a/gb2 heterodimer

**d**gb1a monomer

1 2 3

FIG.14

APPROVED O.G. FIG. CLASS SUBCLASS

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1 atgctgctgc tgctgcttct gcttctcttc ctccgccccc tgggcgctgg cggggctcag 61 acccccaacg tcacctcgga aggttgccag attatacatc cgccctggga aggtggcatc 121 aggtaccgtg gcttgattcg cgaccaggtg aaggccatca atttcctgcc tgtggactat 181 gagattgaat atgtgtgccg gggcgaacgc gaggtggtgg ggcccaaggt gcgcaagtgc 241 ctggccaacg gctcctggac ggatatggac acacccagtc gctgtgtccg aatctgctcc 301 aagtettatt tgaccetgga aaatgggaag gtttteetga egggtgggga eeteecaget 361 ctggatggag cccgggtgga tttccgatgt gaccctgact tccatctggt gggcagctcc 421 cggagcatct gtagtcaggg ccagtggagc acccccaagc cccactgcca ggtgaatcga 481 acgccacact cagaacggcg tgcagtatac atcggggcgc tgtttcccat gagcgggggc 541 tggccggggg gccaggcctg ccagcctgcg gtggagatgg cgctggagga cgttaacagc 601 cgcagagaca tcctgccgga ctacgagctc aagcttatcc accacgacag caagtgcgac 661 ccagggcaag ccaccaagta cttgtatgaa ctactctaca acgaccccat caagatcatc 721 ctcatgcccg gctgcagctc tgtgtccaca ctggtagccg aggctgcccg gatgtggaac 781 cttattgtgc tctcatatgg ctccagctca ccagccttgt caaaccgaca gcggtttcca 841 acgttctttc ggacacatcc atccgccaca ctccacaatc ccacccgggt gaaactcttc 901 gaaaagtggg gctggaagaa gattgccacc atccagcaga ctaccgaggt cttcacctca 961 acactggatg acctggagga gcgagtgaaa gaggctggga ttgagatcac ttttcgacag 1021 agtttcttct cagatccagc tgtgcctgtt aaaaacctga agcgtcaaga tgctcgaatc 1081 atcgtgggac ttttctatga gaccgaagcc cggaaagttt tttgtgaggt ctataaggaa 1141 cggctctttg ggaagaagta tgtctggttt ctcatcgggt ggtatgctga caactggttc 1201 aaaacctatg acccgtcaat caattgtaca gtagaagaga tgactgaggc ggtggagggc 1261 catatcacca cggagattgt catgctgaac cctgccaaca cccgaagcat ttccaacatg 1321 acatcacagg aatttgtgga gaaactaacc aagcggctga aaagacaccc tgaggagact 1381 ggaggcttcc aggaggcacc actggcctat gatgctattt gggccttggc tttggccttg 1441 aacaagacct ctggaggagg tggccgttca ggagtgcgcc tggaggactt taactacaac 1501 aaccagacca ttacagacca aatctaccgg gccatgaact cctcctctt tgagggtgtt 1561 tctggccacg tggtctttga tgccagcggc tcccggatgg catggacgct tatcgagcag 1621 ctacagggcg gcagctacaa gaagatcggc tactacgaca gcaccaagga tgatctttcc 1681 tggtccaaaa cagacaagtg gatcggaggg tctcccccag ccgaccagac cttggtcatc 1741 aagacattcc gtttcctgtc acagaaactc tttatctccg tctcagttct ctccagcctg 1801 ggcattgttc ttgctgttgt ctgtctgtcc tttaacatct acaactccca cgctcgttat 1861 atccagaatt cccagcccaa cctgaacaat ctgactgctg tgggctgctc actggcactg 1921 gctgttgtct tccctctcgg gctggatggt taccacatag ggagaagcca gttcccgttt 1981 gtctgccagg cccgcctttg gctcttgggc ttgggcttta gtctgggcta tggctctatg 2041 ttcaccaaga tctggtgggt ccacacagtc ttcacgaaga aggaggagaa gaaggagtgg 2101 aggaagaccc tagagccctg gaaactctat gccactgtgg gcctgctggt gggcatggat 2161 gtcctgactc ttgccatctg gcagattgtg gaccccttgc accgaaccat tgagactttt 2221 gccaaggagg aaccaaagga agacatcgat gtctccattc tgccccagtt ggagcactgc 2281 agctccaaga agatgaatac gtggcttggc attttctatg gttacaaggg gctgctgctg 2341 ctgctgggaa tctttcttgc ttacgaaacc aagagcgtgt ccactgaaaa gatcaatgac 2401 cacagggccg tgggcatggc tatctacaat gtcgcggtcc tgtgtctcat cactgctcct 2461 gtgaccatga tcctttccag tcagcaggac gcagcctttg cctttgcctc tctggccatc 2521 gtgttctctt cctacatcac tctggttgtg ctctttgtgc ccaagatgcg caggctgatc 2581 acccgagggg aatggcagtc tgaaacgcag gacaccatga aaacaggatc atccaccaac 2641 aacaacgagg aagagaagtc ccgactgttg gagaaggaaa accgagaact ggaaaagatc 2701 atcgctgaga aagaggagcg cgtctctgaa ctgcgccatc agctccagtc tcggcagcaa 2761 ctccgctcac ggcgccaccc cccaacaccc ccagatccct ctgggggcct tcccagggga 2821 ccctctgagc cccctgaccg gcttagctgt gatgggagtc gagtacattt gctttacaag 2881 tga

FIG.15

APPHOVED O.G. FIG.

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MLLLLLLLFLRPLGAGGAQTPNVTSEGCQIIHPPWEGGIRYRGLIRDQVKAINFLPVDY EIEYVCRGEREVVGPKVRKCLANGSWTDMDTPSRCVRICSKSYLTLENGKVFLTGGDLPA LDGARVDFRCDPDFHLVGSSRSICSQGQWSTPKPHCQVNRTPHSERRAVYIGALFPMSGG WPGGQACQPAVEMALEDVNSRRDILPDYELKLIHHDSKCDPGQATKYLYELLYNDPIKII LMPGCSSVSTLVAEAARMWNLIVLSYGSSSPALSNRQRFPTFFRTHPSATLHNPTRVKLF EKWGWKKIATIQQTTEVFTSTLDDLEERVKEAGIEITFRQSFFSDPAVPVKNLKRQDARI IVGLFYETEARKVFCEVYKERLFGKKYVWFLIGWYADNWFKTYDPSINCTVEEMTEAVEG HITTEIVMLNPANTRSISNMTSQEFVEKLTKRLKRHPEETGGFQEAPLAYDAIWALALAL NKTSGGGGRSGVRLEDFNYNNQTITDQIYRAMNSSSFEGVSGHVVFDASGSRMAWTLIEQ LQGGSYKKIGYYDSTKDDLSWSKTDKWIGGSPPADQTLVIKTFRFLSQKLFISVSVLSSL GIVLAVVCLSFNIYNSHARYIQNSQPNLNNLTAVGCSLALAVVFPLGLDGYHIGRSQFPF VCQARLWLLGLGFSLGYGSMFTKIWWVHTVFTKKEEKKEWRKTLEPWKLYATVGLLVGMD VLTLAIWQIVDPLHRTIETFAKEEPKEDIDVSILPQLEHCSSKKMNTWLGIFYGYKGLLL LLGIFLAYETKSVSTEKINDHRAVGMAIYNVAVLCLITAPVTMILSSQQDAAFAFASLAI VFSSYITLVVLFVPKMRRLITRGEWQSETQDTMKTGSSTNNNEEEKSRLLEKENRELEKI IAEKEERVSELRHQLQSRQQLRSRRHPPTPPDPSGGLPRGPSEPPDRLSCDGSRVHLLYK

FIG. 16

APPROVED O.G. FIG. BY CLASS SUBCLASS DRAFTSMAN	labelling —— 98 kDa	C-gb1a
The first stands were the same than the same than the same that the same than the same that the same than the same that the same than the same that the same than the same	[125 I]CGP71872 photoaffinity labelling  [	N-gb1A
	invitro transcription/translation  []	

MLLLLLAPLFLRPPGAGGAHTPNATSEGCQIIHPPWEGGIRYRGLTRDQV KAINFLPVDYEIEYVCRGEREVVGPKVRKCLANGSWTDMDTPSRCVRICS KSYLTLENGKVFLTGGDLPALDGARADFRCDPDFHLVGSSRSICSQGQWST PKPHCOVNRTPHSERRAVYIGALFPMSGGWPGGQACQPAVEMALEDVNS RRDILPDYELKLIHHDSKCDPGQATKYLYELLYNDPIKIILMPGCSSVSTLV AEAARMWNLIVLSYGSSSPALSNRQRFPTFFRTHPSATLHNPTRVKLFEKW GWKKIATIQQTTEVFTSTLDDLEERVKEAGIEITFRQSFFSDPAVPVKNLKRQ DARIIVGLFYETEARKVFCEVYKERLFGKKYVWFLIGWYADNWFKIYDPS INCTVDEMTEAVEGHITTEIVMLNPANTRSISNMTSQEFVEKLTKRLKRHPE ETGGFQEAPLAYDAIWALALALNKTSGGGGRSGVRLEDFNYNNQTITDQI YRAMNSSSFEGVSGHVVFDASGSRMAWTLIEQLQGGSYKKIGYYDSTKDD LSWSKTDKWIGGSPPADQTLVIKTFRFLSQKLFISVSVLSSLGIVLAVVCLSF NIYNSHVRYIONSOPNLNNLTAVGCSLALAAVFPLGLDGYHIGRNQFPFV CQARLWLLGLGFSLGYGSMFTKIWWVHTVFTKKEEKKEWRKTLEPWKLY ATVGLLVGMDVLTLAIWQIVDPLHRTIETFAKEEPKEDIDVSILPQLEHCSS RKMNTWLGIFYGYKGLLLLLGIFLAYETKSVSTEKINDHRAVGMAIYNVA VLCLITAPVTMILSSQQDAAFAFASLAIVFSSYITLVVLFVPKMRRLITRGE WQSEAQDTMKTGSSTNNNEEEKSRLLEKENRELEKIIAEKEERVSELRHQLQ SROOLRSRRHPPTPPEPSGGLPRGPPEPPDRLSCDGSRVHLLYK

FIG.18A

APPROVED O.G. FIG.
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O.G. FIG.	CLASS SUBCLASS	
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1 atgttgctgc tgctgctact ggcyccactc ttcctccgcc ccccgggcgc gggcgggggcg 61 cataccccca acgccacctc agaaggttgc cagatcatac acccgccctg ggaagggggc 121 atcaggtacc ggggcctgac tcgggaccag gtgaaggcta tcaacttcct gccagtggac 181 tatgagattg agtatgtgtg ccggggggag cgcgaggtgg tggggcccaa ggtccgcaag 241 tgcctggcca acggctcctg gacagatatg gacacaccca gccgctgtgt ccgaatctgc 301 tccaagtctt atttgaccct ggaaaatggg aaggttttcc tgacgggtgg ggacctccca 361 gctctggacg gagcccgggc ggatttccgg tgtgaccccg acttccatct ggtgggcagc 421 tcccggagca tctgtagtca gggccagtgg agcaccccca agccccactg ccaggtgaat 481 cgaacgccac actcagaacg gcgcgcagtg tacatcgggg cactgtttcc catgagcggg 541 ggctggccag ggggccaggc ctgccagccc gcggtggaga tggcgctgga ggacgtgaat 601 agccgcaggg acatcctgcc ggactatgag ctcaagctca tccaccacga cagcaagtgt 661 gatccaggcc aagccaccaa gtacctatat gagctgctct acaacgaccc tatcaagatc 721 atccttatgc ctggctgcag ctctgtctcc acgctggtgg ctgaggctgc taggatgtgg 781 aacctcattg tgctttccta tggctccagc tcaccagccc tgtcaaaccg gcagcgtttc 841 cccactttct tccgaacgca cccatcagcc acactccaca accctacccg cgtgaaactc 901 tttgaaaagt ggggctggaa gaagattgct accatccagc agaccactga ggtcttcact 961 tcgactctgg acgacctgga ggaacgagtg aaggaggctg gaattgagat tactttccgc 1021 cagagtttct tctcagatcc agctgtgccc gtcaaaaacc tgaagcgcca ggatgcccga 1081 atcatcgtgg gacttttcta tgagactgaa gcccggaaag ttttttgtga ggtgtacaag 1141 gagcgtctct ttgggaagaa gtacgtctgg ttcctcattg ggtggtatgc tgacaattgg 1201 ttcaagatct acgacccttc tatcaactgc acagtggatg agatgactga ggcggtggag 1261 ggccacatca caactgagat tgtcatgctg aatcctgcca atacccgcag catttccaac 1321 atgacatccc aggaatttgt ggagaaacta accaagcgac tgaaaagaca ccctgaggag 1381 acaggagget tecaggagge accgetggee tatgatgeea tetgggeett ggeactggee 1441 ctgaacaaga catctggagg aggcggccgt tctggtgtgc gcctggagga cttcaactac 1501 aacaaccaga ccattaccga ccaaatctac cgggcaatga actcttcgtc ctttgagggt 1561 gtctctggcc atgtggtgtt tgatgccagc ggctctcgga tggcatggac gcttatcgag 1621 cagcttcagg gtggcagcta caagaagatt ggctactatg acagcaccaa ggatgatctt 1681 tcctggtcca aaacagataa atggattgga gggtcccccc cagctgacca gaccctggtc 1741 atcaagacat tccgcttcct gtcacagaaa ctctttatct ccgtctcagt tctctccagc 1801 ctgggcattg tcctagctgt tgtctgtctg tcctttaaca tctacaactc acatgtccgt 1861 tatatccaga actcacagcc caacctgaac aacctgactg ctgtgggctg ctcactggct 1921 ttagctgctg tcttcccct ggggctcgat ggttaccaca ttgggaggaa ccagtttcct 1981 ttcgtctgcc aggcccgcct ctggctcctg ggcctgggct ttagtctggg ctacggttcc 2041 atgttcacca agatttggtg ggtccacacg gtcttcacaa agaaggaaga aaagaaggag 2101 tggaggaaga ctctggaacc ctggaagctg tatgccacag tgggcctgct ggtgggcatg 2161 gatgtcctca ctctcgccat ctggcagatc gtggaccctc tgcaccggac cattgagaca 2221 tttgccaagg aggaacctaa ggaagatatt gacgtctcta ttctgcccca gctggagcat 2281 tgcagctcca ggaagatgaa tacatggctt ggcattttct atggttacaa ggggctgctg 2341 ctgctgctgg gaatcttcct tgcttatgag accaagagtg tgtccactga gaagatcaat 2401 gatcaccggg ctgtgggcat ggctatctac aatgtggcag tcctgtgcct catcactgct 2461 cctgtcacca tgattctgtc cagccagcag gatgcagcct ttgcctttgc ctctcttgcc 2521 atagttttct cctcctatat cactcttgtt gtgctctttg tgcccaagat gcgcaggctg 2581 atcacccgag gggaatggca gtcggaggcg caggacacca tgaagacagg gtcatcgacc 2641 aacaacaacg aggaggagaa gtcccggctg ttggagaagg agaaccgtga actggaaaag 2701 atcattgctg agaaagagga gcgtgtctct gaactgcgcc atcaactcca gtctcggcag 2761 cageteeget eceggegeea eceaecgaea eceeeagaac ectetggggg eetgeeeagg 2821 ggaccccctg agccccccga ccggcttagc tgtgatggga gtcgagtgca tttgctttat

FIG.18B

APPROVED O.G. FIG.

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1	atgctgctgc	tactactage	gccactctic	ctccgccccc	cgggcgcggg (	cggggcgcag
61	2000002200	ccacctcada -	addttoccao	arcaracacc	Cuccciuuua -	ayyyyycaic
121	aget accord	מככלמאכדכם	adaccaddi.u	aduultatta	acticciyee	agtggactat
181	gagattgagt ctggccaacg	actectagae	adatatodac	acaccauct.	actulutud	aatttqttt
201	2 2 2 t C t t 2 t t	taaccctaaa	AAATOOOAAO	CH L L L.C.C.L.Ura	t.uuutuuuu	CCCCCage
261	ctogacogao	cecaaataaa .	TT LCCQQ LQ L	udccccqaci	licalitygi	gggcugctcc
1/21	caaaacatct	of act cacco	ccam ggage.	at.t.t.taayt	CCCactycca	ggtguutegu
481	acoccacact	cadaacddcd	cacaatatac	allygygeac	Lycallactur	909099999
541	tggccagggg	gccaggcctg	ccagcccgcg	grggagargg	cyclyyayya	caantntnat
601	cgcagggaca	tcctgccgga	ctatgagete	adgeteatee	accacyacay	caagatcatc
661	ccaggccaag	ccaccaagta	cctatatgag	ctactaceta	acqueectue	catgiceace
721	cttatgcctg	gctgcagctc	tgtctccacg	ciggiggerg	caaaccooca	acatttccc
781	ctcattgtgc	tttcctatgg	ctccagcica	ctagecetye	ctaccogcat	gaaactcttt
841	actttcttcc	gaacgcaccc	accagecaca	atcoacca	ccactgagg	cttcacttca
901	gaaaagtggg	gctggaagaa	garigerace	acctageaga	ttgagattac	tttccaccaa
961	actctggacg	acctggagga	acgagigaag	gayyetyyaa	accoccado	toccoaato
1021	agtttcttct	cagatccagc	igigeegee	caassattt	tttataaaat	atacaaggag
1081	atcgtgggac	ttttctatga	gactyaaycc	ctcattagat	antatactaa	caattootto
1141	cgtctctttg	ggaagaagia	cyttiggtte	ataataaa	taactaaaac	aataaaaaac
1201	aagatctacg cacatcacaa	accclicial	catactaaat	cctoccaata	ccacaacat	ttccaacata
1261	acatcccagg	Cigagaligi	catyctydat	aaggactga	aaagacaccc	tgaggagaca
1321	ggaggcttcc	adiliyiyya	gadactaacc	natoccatct	agacttaac	actggccctg
1381	aacaagacat	ayyayycacc	caaccattct	gatgeeatee	tggaggactt	caactacaac
1441	aaccagacca	ttaccaacca	aatctaccoo	ggtgtgeget	cttcatcctt	taaagatatc
1501	tctggccatg	taatatttaa	taccaacaac	totogataa	catagacact	tatcgagcag
1001	cctcagggtg	acaactacaa	gecagegge	tactatgaca	acaccaagga	tgatctttcc
1601	tggtccaaaa	cadataaatd	nattonanno	tocococaa	ctgaccagac	cctqqtcatc
	and a state of	acttectate	acadaaacto	tttatctccg	tctcagttct	ctccagcctg
1741 1801	aayacactcc	tanctuttut	ctatctatco	tttaacatct	acaactcaca	tgtccgttat
1961	atccagaact	cacancecaa	cctgaacaac	ctaactacta	tagactactc	actggcttta
1921	actactatet	teceetaaa	acticaataat	taccacattg	ggaggaacca	gtttcctttc
1981	ntctaccaaa	cncacctcta	act.cct.agac	ctgggcttta	gtctgggcta	cggttccatg
20/1	ttcaccaaga	tttaataaat	ccacacagaga	ttcacaaaga	aggaagaaaa	gaaggagtgg
2101	aggaagactc	tagaacccta	aaaactatat	, qccacagtgg	gcctgctggt	gygcatygat
2161	atceteacte	traccatita	- acadatcato	ı qaccetetqe	accggaccat	tydydcaili
2221	accaaaaaaa	aacctaagga	agatattgac	gicicialic	Lgccccayet	ggagcallyc
2281	l ancticcanga	agatgaatac	: ataacttaac	: attttctatg	gttacaaggg	gatgatgatg
23/11	Lictortogoaa	tetteett <b>ac</b>	: t.t.atgagacc	: aagagtgtgt	ccactgagaa	galcaalgal
2401	l caccagacta	tagacatago	tatctacaat	gtggcagtcc	tgtgcctcat	cactgctcct
2461	l atraccatga	ttctatccac	ı ccaqcaqqat	geageetttg	cctttgccic	littigicala
2521	l attttctcct	: cctatatc <b>ac</b>	: tcttqttqtç	g ctctttgtgc	ccaagatgcg	caggctgatc
2581	lacccgaggg	i aatgoca <b>gt</b> o	agaggcgcag	ı qacaccatga	agacagggtc	atcyaccaac
264	l aacaacdadd	aggagaagto	c coggetatte	g gagaaggaga	accgtgaact	. ggaaaagatc
270	l attoctoaga	aagaggagco	ı tqtctctgaa	a ctgcgccatc	: aactccagtc	teggeageag
276	1 ctropotice	: aacaccacco	accgacacco	c ccagaaccct	. ctgggggcct	: gcccagggga
282	1 coccetaaac	r concordance	a acttaacta	t qatqqqaqto	: gagtgcattt	: gctttataag
288	1 taannatano	n otaaooaaa	i acaddccad	t agggggagg	i aaaqqqagag	g gggaagggca
294	l agggactcac	n daadcaddd	a atccccatc	c ccagctggga	a agaacatgci	alccaalcic
300	1 atotottota	a aatacatoto	- cocotataa	a ttctaaacta	ı attiqggici	, Cicalaccic
306	1 tgggaaacag	g acctttttc1	t ctcttactg	c ttcatgtaat	: tttgtatcac	ctcttcacaa
				_		

FIG.19A

3121					gctgcctcct	
3181	actgcatctt	tctcttccca	tgcaacaccc	tcttctagtt	accacggcaa	cccctgcagc
3241	tcctctgcct	ttgtgctctg	ttcctgtcca	gcaggggtct	cccaacaagt	gctctttcca
3301					tttccatctt	
3361					ctttgggagc	
3421					cacgctcagc	
3481					gtacacacgc	
3541					tgcattcaca	
3601					gtaggcatgt	
3661					tgtttatcca	
3721					aatcatggta	
3781					ttccccaatt	
3841					tctgctcaga	
3901					atcatcttct	
3961					aaataagtgg	
4021					caaaggaagg	
4081					gtccctttca	
4141	tctcttgggg	aaggatctcc	ccgaatctca	ataaaccagt	gaacagtgtg	actcggaaaa
4201	aaaaaaaaa	aaaaaaaaa	a			

FIG.19B

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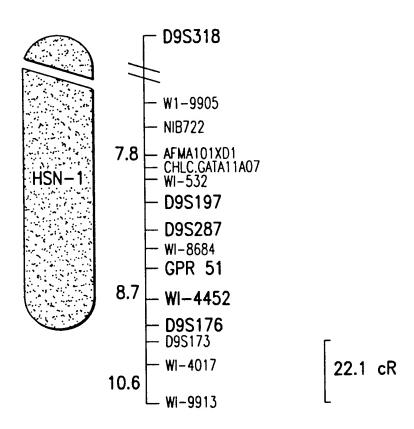
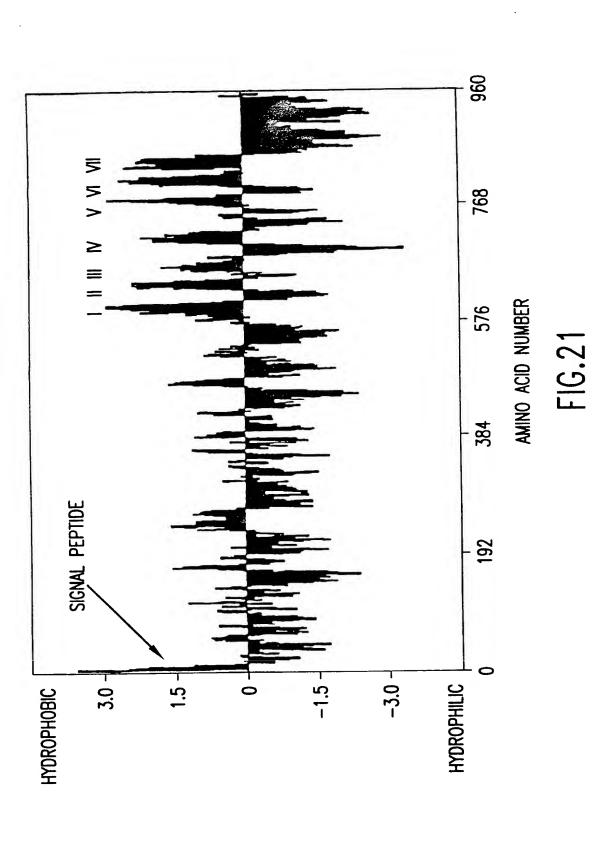


FIG. 20

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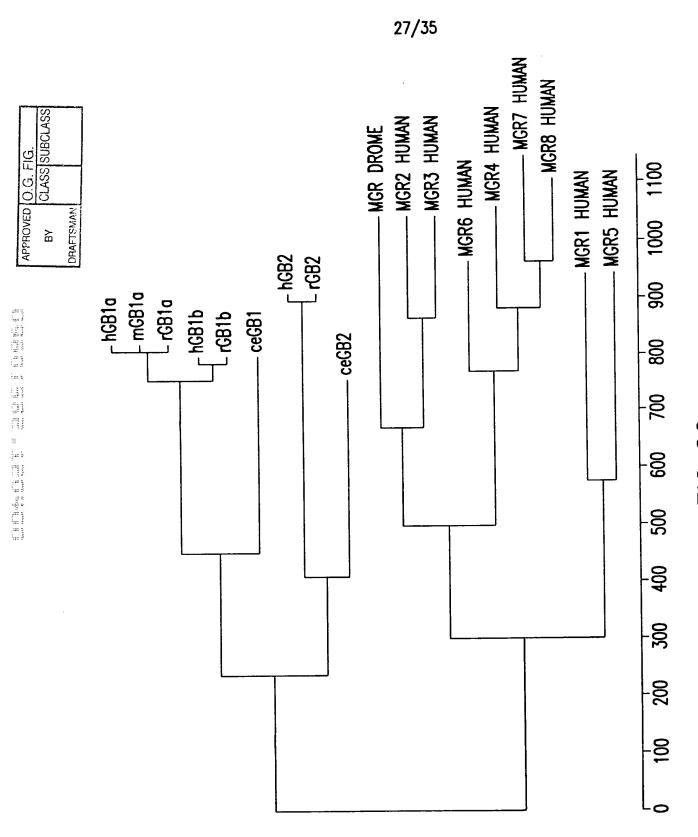


FIG. 22

APPROVED O.G. FIG.
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# COILED—COIL DOMAIN IN C—TERMINUS OF 9519 AND HG20 MEDIATING HETERODIMERIZATION

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gbi ....wosea.odtwktgsstnnneeek...srllek..enrelekiiaekeervselrholosroolrsrrhpp hg20 onrrfoftonokkedsktstsvtsvnoastsrleglosenhrlrwkiteldkdleevtwolodtpektiyikon

FIG.23

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TRACTORY TRANSPORTER

APPROVED O.G. FIG.
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≓ !	-PA		29/35		
10 20 30 40 50 60 70 80 90 100 JR MLLLLLLAPLFLRPPGAGGAQTPNATSEĞCQ11HPPWEGG1RYRGLTRDQVKAINFLPVDYE1EYVCRGEREVVGPKVRKCLANGSWTDMDTLSRCVR1CSKSYLTL	1-B1	ENCKVFL TGCOL PADDGARMDFRCOPDFHL VGSSRS I CSCGCWSTPKPHCQVNRTPHSERRAVY I CAL FPNSGGMGGAGGPAVEMALEDVNSRAD I EDGTELJKL I HEDGKGDFGA 	230 240 320 330 340 320 330 340 320 340 340 340 320 320 330 340 340 340 340 340 340 340 340 34	350 360 370 380 390 400 410 420 430 440  OSEPSEPAVPVRNUKRODARI I VOLFYEITEARKYFÖLVYKERUFÖKKYVWFLLIGWYADNINFK I YDPSINCINDEMTEAVECENITTEI VALLYNDARI I VOLFYEITEARKYFÖLVÄTSKAN TOLOMORIA (SERVENIT I VOLFYEITEARKYLÖDANHHOLNGRRYVALI VOLFY (SAMT) SAMT TOLOMORIA I VOLFYMIL SAMT TOLOMORIA (SAMT) SAMT TOLOMORIA I VOLFYMIL VOLFYMIL SAMT TOLOMORIA I VOLTY SAMT TOLOMORIA S	450 460 470 480 490 500 510 520 520 530 540 550 560 560 510 520 530 540 550 550 560 560 560 570 520 570 570 550 560 560 570 570 570 570 570 570 570 570 570 57
Human GABA-BlaR	C.elegans GABA-B1 C.elegans GABA-B2 Human GABA-B2	110 ENGKVFLTGGDLPADDGAF MFVRSSWLLDMGTI 	230 240 ATKYLYELLYNOBIRITID AMOQLYDFLYKPPTRAMI GMKALFDLIJASRPRPVAT GLKAFYDAJIKYCPNHLMVI	350 IQSEJF SDPAVPVKNUKROD IQSEJYGDBTDAMKNTUGROD PRYALIVRGD ESF SNOPCTSVKKLIKGND	450 LTKRL KRHPEE T <u>GGEQEA</u> LTOYF QKD TANV <u>GGEPEA</u> AGDVWNE I TQLDPNNTWR YNNKRSGVGPS-KFH

KECMA, NOKCERPO STVIKTEN-SYBOFILIFISTI I DOYFSOFIAL LHVOSFTFLHKNI I FO-EOPECNNILL I ICCSICOFSUE I CLIPSODI SIISESLED LOHAÄVTILI I DSTTKOWSPPILD-STIITERRAEHISSI I IFLAMOLITALI I I I I INFRYRNHRFITKWSSPNLINNI I I I AGSI CTFASVI MLOLOT--RIVSPOVFIVMLOYTKI WITH IJLGCMLSYASIFLFGLDC--SFVSEKTEETLGTVRTMII 570 580 590 TMS-1 610 620 630 TMS-2 650 660 TDKMICG-SPIADOTL<u>VIKTE</u>R-FLEOKUFISVSVUSSLGIVLAVVCLEFNIYNSHVRYIONSOPVLNNLTAVGCSLALAAVEPLGUDG--YHUGRNOFPVC THE REPORT OF SECUL SAME SAME SAME SHAPE DTIRFCGSEPPADKTIJJLEOLB-K<u>ISLPJ</u>YSILBAJTILCMIMASAELFINIKNRNOKL<u>IKMSSP</u>YMNNLJ 610

FGAMESKTWRVHSIFTNI---IRMDRRAIKDSKUFIIILGILUFIDIGMUNTWAFNSPFSYTVEOFKFLIFSARRÄNIMIINEVEKONSSFSGVFGAVUYAMKGMUMILGGFLAWFTRHV FGAMEAKTWRVHAIFKNI---VRAKKKIIKDOKULVINGSMULIDUGIUIGWOAMDBURRTVEKYSMEPDPAGROISIIRBULEHOENTHMTIWUGIVYAYKGULMFGGFLAWETRNV YGSMFITMINMWHTVFTKKEEKKEWRKTLEPWALMATNGCLLVGWOVLTLAIMOIVÖPLHATIIETBAKEEPKEDIDVSIILBOLEHOSBRKMNTMIGJFYGYKOLLI <u>YGSMFJARANIJÍVHR</u>NGATENQOLASPROPÍSSSRFTRVÍRJAALÍTAVOUJFVCFVINVLÍ<u>DPLH</u>LÍTE OKFPLFÄDSELEÜEMÍRAFJAGGGGBNOGEVINIĞI INGFROF 760 C

750

740

720 TMS-4 730

902

9

-----EJQDTMKTQSSTNNNEEEKJSRLLEKENR -----EIQLNGNVGPGVMSKVDOK}-----NWPALNDSKYIGTSVYCCVMSVLGLSTSVILQE-RVNEMFSLASFF-VIFFSTFLITLCLVFVPRVRFFLELCCIGS---------------------------------SI<u>PALNDSKYIGMSVY</u>NVGIMCIIGAAVSFLTRD-QPNVQFCIVALV-I<u>[[F</u>CST]I<u>[TLCLVFVPK</u>LITL]RTNPDAATQNRRFQFTQNQKKEDSKTSTSVTSVNQASTSRLEGLQSENH STEK<u>IND) RAVĞMA I YNVAVI CIJÎ I APVITM ÎL</u>SS-Q<u>ÖDAME AFIASLIA-Î VESSY ÎJTL VVLF VER</u>MERLIÎTRGEWQS ---KLRF<u>ÎNDSEFINGLA I YNVAVI</u>MTÎDVÎ APVIVTLÎ I HCKVDANÊ AFIISLÎ ÎSVL I CÎ<u>YÎ</u>SVGL Î YGÊKÎ ÎBHÎÎKVPPSAD ---850 TMS-7

-PPEPPDRL SCDGSRVHLL YK--ELEKIIAEKEERVSELRHOLOSROOLRSRRHPPTPPEPSGGLPRG--920

RLRMKITELDKDLEEVTMQLQDTPEKTTYIKQNHYQELNDILNLGNFTESTDGGKAILKNHLDQNPQLQWNTTEPSRTCKDPIEDINSPEHIQRRLSLQLPILHHAYLPSIGGVDAS

CVSPCVSPTASPRHRHVPPSFRVMVSGL

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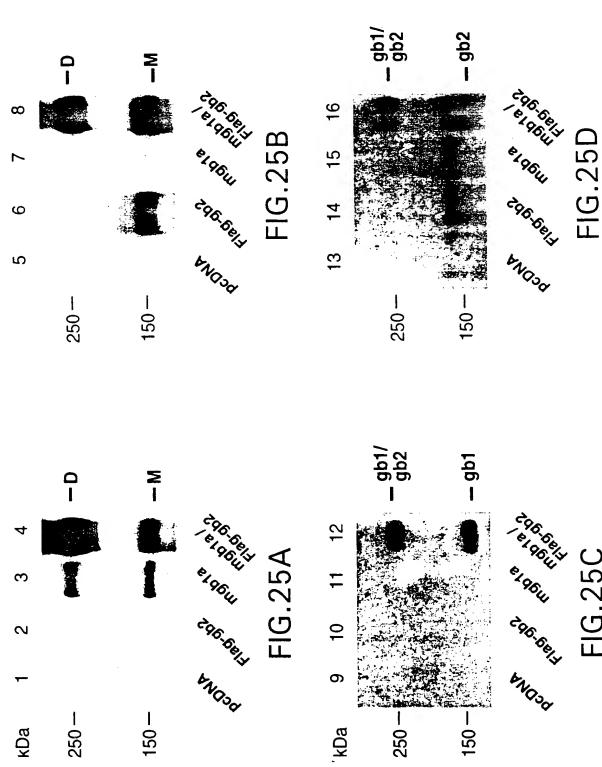


FIG.26A-1

MCABAb10 MLLLLLLL LFLRPLGAGGAOTPNVTSEGCOIIHPPMEGGIRYRGL IRDQVKAINFLPVDYE IEYVCRGEREVVGPKVRKCLANGSWTDMDTPSRCVRICSKSYLTLENGKVFLTGGDLP:119 hGABAb10 MLLLLLLAPLFLRPPGAGGAOTPNATSEGCOIIHPPMEGGIRYRGL IRDQVKAINFLPVDYE IEYVCRGEREVVGPKVRKCLANGSWTDMDTPSRCVRICSKSYLTLENGKVFLTGGDLP:120 hGABAb2 M. AS. AS. AS. AS. AS. AS. AS. AS. AS. AS	MCABABIO ALDGARVOFRCOPDFHLVGSSRSICSQQGWSTPKPHCQVNRTPHSERRAVYICALFPMS. GGWPG. GQACQPAVEMALEDANSRRD. ILPDYELKLIHHD. SKQDPQQATKYLYELLY:23*  hGABABIO ALDGARVOFRCOPDFHLVGSSRSICSQQWSTPKPHCQVNRTPHSERRAVYICALFPMS. GGWPG. GQACQPAVEMALEDANSRRD. ILPDYELKLIHHD. SKQDPQQATKYLYELLY:23*  hGABAB2 LL. LPLAPGAWGWA. RGAPRP. PPSSP. PLSIMCLMPLTKEVAKGSIGRGVLPAVELAIEQI RNESLLRPYFLDLRLYO. TEQDNAKGLKAFYDAIK:12*  mG1uRi VIIGALFSVHHQPPAEKVPERKCGEIREQMGIQR. VEAMFHTLDKINADPVLLPNITLGSE. IRB. SCWHSSVALEQSIEFIRDSLISIRDEKDGI. NRCLP:142*  Livk. VVGAM. SGPV. AQNGIME. FTGAEQAVADINAKGGIKGDKLVGVE. YDD. AC. DPRQAVANKVNN: 67*  Livb VVGAM. SGPV. AQNGDQE. FTGAEQAVADINAKGGIKGDKLVGVE. YDD. AC. DPRQAVANKVNN: 67*	MCABADIO NO. PINIIILMPG CSSVSTLVAEAARNANN. LIVUSYGSSSTALSNRORFPTFFRIHPSATLHNPTRVM.LFEKWGMKKIATIQOTTEVFTS. TÜDDLEERVKEAGI: 33: hGABADIO NO. PINIIILMPG CSSVSTLVAEAARNANN. LIVUSTGSSSTALSNRORFPTFFRIHPSATLHNPTRVM.LFEKWGMKKIATIQOTTEVFTS. TÜDDLEERVKEAGI: 335 hGABADIO NO. PNHLMVFGSVGTSIIMESLOGWN. LVOLGFAATITPVLADKKKMPYFFRTMPSDNAVVPAILMS. LLKHYGMKRVGTLTQDVORFSE. VRNDLTGVLYGEDI: 224 mG1uR1 DCOSLPPGRTKKPTMGSVGTSVGSSVATQVONLLQLFDTPOTAYSATSIDLSDKTLMYVPSDTLQARAM DIVKRYNMTYVSAV.HTGONYGESGNDAFKELAAGEGI: 253 LIVK DG. INTEDEGILMISPGATAPELTORG. MCHINRTAGLDSSOGPTAAMTILETVKP.QR[AII.HDKQOYGE.GLARSVQDGL: 185 LIVK DG. IIATVI.GHLCSSISTOPAS. DIYEDEGILMITPAATADELTORG. MCHINRTAGLDSSOGPTAAMTILETVKP.QR[AII.HDKQOYGE.GLARAVQDGL: 162 LIVBP
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ALNP: 431 ALNP: 435 PLSS: 324 DTN: 362 LVTM: 271 LVTK: 248	A. FDASGSRWA: 534 A. FDASGSRWA: 535 A. FR. NGERMG: 424 A. FDE KODAFO: 477 A. FOEKODAFO: 477 A. FOEKODLKP: 351 A. WDE KODLKP: 326	33/35
MGABADIO EIITEROSFISOPAVPVKN LIKRODARII INGLEYET EARKVFGEVYKERLFÖKKTVWFLIGWYADNMFK TYDPSINCTVEEM.TEANEGHITTE IVMLNP:433 hGABADIO EIITEROSFISOPAVPVKN LIKRODARII INGLEYET EARKVFGEVYKERLFÖKKTVWFLIGWYADNMFK TYDPSINCTVOEM.TEANEGHITTE IVMLNP:433 hGABADZ EIISDTESFSNDPCTSVKK LKGNDVRII INGLEYET EARKVFGEYEENNAGSKYOWIIPGWYEPSMWEQ VHTEANSSRCLRKNL.LAANEGYIGVD FEPLSS:324 mGIURI CIJAHSDKIYSN AGENGFDRLIERLFREI PKARVVVGFGEM TVRGLISAM RRIGNVGEFSLIG SDGMADRDEVIEGYEVEANGGIT IKLOSPEVRSFDDYFLKLRIDTN:362 Livk KAANANVVFFDGITAGENOFSALI ARLKKENIDFVYYGGYYPENGOMLROA RSVGLKTGF. NG PEG VANSLSNIAGENAEG	MCABAB10 ANTRSISNMTSQEFVEKLTKRLKRHPE ETGGF GEAPLAYD ANNALALALNK TSGGGRSGVRLEDFNYNNOTITDQIYRAMNSSFEGVSGHWN FDASGSRMA:534 hGABAB10 ANTRSISNMTSQEFVEKLTKRLKRHPE ETGGF GEAPLAYD ANNALALNK TSGGGRSGVRLEDFNYNNOTITDQIYRAMNSSFEGVSGHWN FDASGSRMA:535 hGABAB2 KQIKTISGKTPQQYEREYNN KRSGV GPSKF HG. YAYD GIMVIJAKTLORAMETLHASSRHQ.RICDFNYTDHTLGRIILNAMNETNFFCVTGOWN FR.NGERMG:424 mG.IUR1 TRNPWFPEFWOHRFQCRLPGHLLENPNFKRICTGNESLEENYYQDSKNGFVINALINYAMALQSLATALERTGSDEPLAL.VKDLKANG. ANTVIGPLN WDEKGDLKG:351 LIVK PK. RYD. QDPANGIV DAIKAK.KQDPSGMFV.WITYAMALQSLOAGLNQ.SDDPAEI.AKYLKANSVDTVNGPLNWDEKGDLKG:326 11.VBP PK. NYD. QVPANKPIV. DAIKAK.KQDPSGMFV.WITYAMALQSLOAGLNQ.SDDPAEI.AKYLKANSVDTVNGPLT	mCABAbia WTL IE       QLCGGSYKKIGYYD       STKDDLS WSKTDKWIGGS       PPAD       575         hCABAbia WTL IE       QLCGGSYKKIGYYD       STKDDLS WSKTDKWIGGS       PPA       575         hCABAb 1 WTL IE       QLCGGSYKKIGYYD       AVADTLE IINDTIRFOGS       PPAD       475         hCABAb 2 TIKFT       QFQDSREVKVGEYN       AVADTLE IINDTIRFOGS       PPKDRTIILEQLR       475         mCIURI       RYDIMNLQYTEANRYDYVHVGTWHECVLNIDDYKIQMNKSGVVRSVCESPCLKGQIKVIRKGEVSCCWICTROKENEYVQDEFTCKACDLGWPPNADLTGCEPIPVRY:585       369         LIVK       FDF       GVFQ       WHANGT       ATDAK         IIVBP       FEF       GVFQ       WHANGT       ATDAK

# FIG.26A-2

e la mille pranca e calec.

34/35

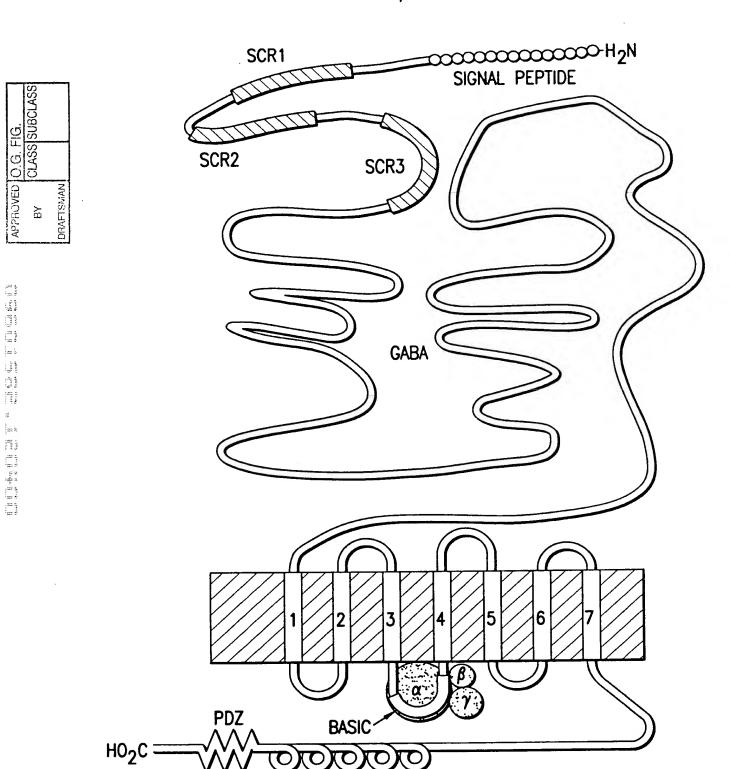


FIG.26B

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CLASS SUBCLASS	ВУ

39	50	57 100	95	149	106	107	
KMR RLITRGEW QSETQDTMKTGSS. TNNNEEEKSRL LEKE: PKMR RLITRGEW QSEAQDTMKTGSS. TNNNEEEKSRL LEKE:	ITLRINPDAAITONRRFOFTONOKKEDSKTSTSVTSVNOASTSRLEGLOSE:	NRJELEKIJAEJKEERVSEJ NHRLRMKITELDNDLEENTMQLQDTPEKTTYIKQNHYQELNDILNLGNFT: ▲↑	LRHOLOSROOL RSRRHPP TPPDPSGGLPRGPSEPPDRLS:	ESTOGGKA ILKNIH DONPOLOWNTTEPSRITCKDPIEDI. NSPEHIORRUS:	CDGSRV	SPCVSPTAS	
mGABAb1a hGABAb1a	hGABAb2 mGABAb1a	hGABAb1a hGABAb2	mCABAb1a	hGABAb I a hGABAb2	mGABAb10	hCABAb1a	40000II

### FIG.27